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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/029,677

DATE: 05/16/2002

TIME: 13:22:07

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05162002\J029677.raw

3 <110> APPLICANT: Westphal, Ryan S.	
⊿ Feder, John N.	
5 Ramanathan, Chandra S.	
6 Mintier, Gabriel A. AND MOLECULES AND POLYPEPTIDES FO	OR A HUMAN CATION
6 Mintier, Gabriel A. 8 <120> TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND POLYPEPTIDES FO	
CHANNEL	
o POLYPEPTIDE	
120 BILE PEFFRENCE: D0187NP	
12 CIAON CUPDENT APPLICATION NUMBER: 10/025/51	
The state of the position will include the court of the c	
15 /150 DRIOR APPLICATION NOMBER. 00 0-7	
16 <151> PRIOR FILING DATE: 2000-12 21	
10 (160) NUMBER OF SEO 1D NOS: 24	
20 <170> SOFTWARE: PatentIn version 3.0	
22 <210> SEQ ID NO: 1	
23 <211> LENGTH: 2186	
24 <212> TYPE: DNA	
25 <213> ORGANISM: Homo sapiens	
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29 <222> LOCATION: (20)(2011)	•
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32 <221> NAME/KEY: misc_feature	
33 <222> LOCATION: (2150)(2150)	
34 <223> OTHER INFORMATION: Wherein in equals 11,	
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39 Met Till Gld Lys 110	
40 and got got age age got age	100
40 42 cca gcc aat aat cac aac cat cat gca cct cct gcc atc aag gcc aat 42 pro Ala Asn Asn His Asn His Ala Pro Pro Ala Ile Lys Ala Asn 43 Pro Ala Asn Asn His Asn His His Ala Pro Pro Ala Ile Lys Ala Asn	
43 Pro Ala Asn Asn His Ash His his his Ala 20 25	
44 15 200 and coa cac tet gea get gac	148
46 ggc aaa gat gac cac agg aca agc agg cod odd 11 Ala Asp 47 Gly Lys Asp Asp His Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp	
47 Gly Lys Asp Asp His Arg Thi Ser Ser May 10	
48 30 de la cara eta goa gac gig gat goc coa	196
48 30 55 50 gat gac acc tcc tca gaa ctg cag agg ctg gca gac gtg gat gcc cca 51 Asp Asp Thr Ser Ser Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro 55	
51 Asp Asp Thr Ser Ser Glu Lea Gli Ary 255	
52 45 50 50 are agg ata get egg etg ggg atc	244
54 cag cag gga agg agt ggc ttc cgc agg atd gcc ogc of San	
55 Gln Gln Gly Arg Ser Gly File Alg Mig 20 75	0.00
56 60 05 and gag gag gag cct agg cct	292
58 atc aga gaa tgg gcc aac aag aat tte ega gag gag gag. Fro Arg Pro 59 Ile Arg Glu Trp Ala Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro	
59 Ile Arg Glu Trp Ala Ash Lys Ash Tho 85	
60 80	

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Output Door I (240
62 gac tca ttc ctc gag cgt ttt cgt ggg cct gaa ctc cag act gtg acc 63 Asp Ser Phe Leu Glu Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr	340
95	388
64 95 100 66 aca cag gag ggg gat ggc aaa ggc gac aag gat ggc gag gac aaa ggc 66 aca cag gag ggg gat ggc aaa ggc gac aag gat ggc glu Asp Lys Gly	
66 aca cag gag ggg gat ggc aaa ggc gac aug gac ggc Glu Asp Lys Gly 67 Thr Gln Glu Gly Asp Gly Lys Gly Asp Lys Asp Gly Glu Asp Lys Gly 115	
67 Thi Gir Gir 317 1 1 120	436
68 110 115 70 acc aag aag aaa ttt gaa cta ttt gtc ttg gac cca gct ggg gat ttg 70 acc aag aag aaa ttt gaa cta ttt gtc ttg gac cca gct ggg gat ttg	450
70 acc aag aag aaa ttt gaa cta ttt gte ttg gae dda gob 333 Sap Leu 71 Thr Lys Lys Phe Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu 130 135	
71 Thr Lys Lys Lys File of 235	484
72 123 at a coc at a citatac aad 199	404
74 tac tac tgc tgg cta ttt gtc att gcc atg ccc geb 557 75 Tyr Tyr Cys Trp Leu Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp 150	
75 Tyr Tyr Cys Trp Leu Pie Val 116 115 150	
76 140 145 ttg agt gac cta cag aaa ggc tac	532
78 tgc ctg ctg gtg gcc aga gcc tgc ttc agt gdc ctd chy 79 Cys Leu Leu Val Ala Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr 165	
70 Cyc Lou Leu Val Ala Ary Ala Cys Inc 555 1	
79 Cys neu	580
80 160 103 82 tac ctg gtg tgg ctg gtg ctg gat tat gtc tca gat gtg gtc tac att 82 tac ctg gtg tgg ctg gtg ctg gat tat gtc tca gat gtg gtc tac att	
82 tac ctg gtg tgg ctg gtg ctg gat tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg ctg gat tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg ctg gat tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtc cca gas 313 5 82 tac ctg gtg tgg ctg gtg tat gtg tac	
180 175 180 180 185	628
of the car and the	020
86 gcg gac ctc ttc atc cga ttg cgc aca ggt ttc ccg gar 87 Ala Asp Leu Phe Ile Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu	
87 Ala Asp Leu Phe Tie Arg 200	676
88 190	676
90 ctg gtc aaa gat acc adg aaa ccg arg Asp Asp Tyr Ile His Thr Leu	
91 Leu Val Lys Asp Thr Lys Lys Leu My 131 215	
92 205 210 210 213 94 cag ttc aag ctg gat gtg gct tcc atc atc ccc act gac ctg atc tat 94 cag ttc aag ctg gat gtg gct tcc atc atc ccc act gac ctg atc tat	724
94 cag ttc aag ctg gat gtg gct tcc atc atc gtc gcb gcb leu Ile Tyr	
or all the Lye Lell ASD val Ala Sel 110 110 110 225	
95 GIR PRE LYS BER 135 225 230 230 230	772
96 220 225 98 ttt gct gtg gac atc cac agc cct gag gtg cgc ttc aac cgc ctg ctg 98 ttt gct gtg gac atc cac agc cct gag gtg cgc ttc aac cgc ctg ctg	
on pho Ala Val ASD IIE HIS SEL PIO GIA (42)	
240 245 250 250 240	820
100 the tett day day and and and the acc	020
102 cac ttt gcc cgc atg ttt gag ttc ttt gac cgg ded 343 103 His Phe Ala Arg Met Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr	
103 His Phe Ala Arg Met Phe 324 260 265	0.50
104 255	868
104 . 255 . 200 106 aac tac cct aac atc ttc cgc atc agc aac ctt gtc ctc tac atc ttg 106 aac tac cct aac atc ttc cgc atc agc aac ctt gtc ctc tac atc ttg 107 Asn Tyr Pro Asn Ile Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu 275 . 280	
107 Asn Tvr Pro Asn Ile Phe Alg Ile Bel 1881 -	
108 270 275	916
108 270 273 110 gtc atc atc cac tgg aat gcc tgc atc tat tat gcc atc tcc aaa tcc 110 gtc atc atc cac tgg aat gcc tgc atc tat tat gcc atc tcc aaa tcc 111 Val Ile Ile His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser 290 295	
111 Val Tle Ile His Trp Asn Ala Cys Ile Tyr Tyr Ala Ile 801 -/-	
112 285 290 290 atc act gac cct	964
114 ata ggc ttt ggg gtc gac acc tgg gtt tac dea all and a sport at a ggc ttt ggg gtc gac acc tgg gtt tac dea all and a sport at a sp	
115 Tie Gry File Gry Van 116 310 310	1012
116 300	1012
118 gag tat ggc tac ctg gct agg gad tac atc cat by Leu Tyr Trp Ser 119 Glu Tyr Gly Tyr Leu Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser 325	
119 Glu Tyr Gly Tyr Leu Ala Alg Gra 172 325	4.5.5.0
120 320 the arg gag aga coa coc cot gta aag gat	1060
120 320 320 120 aca ccc cct gta aag gat 122 aca ctg act ctc act acc att ggg gag aca cca ccc cct gta aag gat 120 aca ctg act ctc act acc att ggg gag aca cca ccc cct gta aag gat	
123 Thr Leu Thr Leu Thr Thr Tie Gly Old 1112 - 245	
124 335 340 345 126 gag gag tac cta ttt gtc atc ttt gac ttc ctg att ggc gtc ctc atc	1108
126 gag gag tac cta ttt gtc atc ttt gac ttc ctg dtc 330 yr	

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14	20		~~~	-	atc	gtg	σαа	aat	gtg	ggc	tcc	atg	atc	tcc	aac	c a	τg	aaı	1130
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1	32		365			gag		3/0			a+a	aat	acc	ata	aaa	a c	ac	tac	1204
1	34	qcc	acc	cgg	gca	gag	ttc	cag	gct	aag	all	gat	315	7723	T.37	c H	iis	Tvr	
1	35	Ãlα	Thr	Arq	Ala	gag Glu	Phe	Gln	Ala	Lys	тте	IIO P	Ala	val	шy.	J 1.	110	305	
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1	46	at.t.	ctc	aaq	aat	ctg	cca	gcc	aag	ctc	agg	get	. gay	, alc	1 9C	. C	Thr	Δen	
1	17	Tle	Len	Lvs	Asn	ctg Leu	Pro	Ala	Lys	Leu	Arg	Ala	GIU	1 TT6	3 AT	.a .	T 11T	ASII	
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1	40		~~~			aca	ctc	aaσ	aaa	gtg	cgc	ato	: ttc	cat	t ga	ıt '	tgt	gag	1330
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1	L52		445			gta			a+ =	cta	aaa	cto	a cat	t cc	t ca	ıq	gtc	ttc	1444
-	L54	gct	ggc	cto	, ctg	gta Val	gag	CLY	yıa	Tou	Two	T.A	1 Ar	a Pr	o Gl	Ln '	val	Phe	
-	155	Ala	Gly	, Lei	ı Lev	Val	Glu	ьeu	vai	Leu	пуз	470		<i>-</i>				475	
																			1492
				ggg	g gat	tac	att	tgc	cgc	aaa	ggg	g gad	3 au	- 99	T	70	Clu	atg Met	
	159	Ser	Pro	G1	Asp	Tyr	· Ile	Cys	Arg	Lys	OI.	1101	5 тт	е ст	у п	yЗ	400	Met	
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	160	+ 20	ı atı	at:	t aac	a dad	aac	aaa	ctg	gca	gt	g gt	g gc	t ga	t g	aτ	ggu	gtg Val	1340
	102	meet	, ut.	2 Tl	o T.379	: G111	Ğĺv	Lvs	Leu	Ala	. Va.	L Va	l Al	a As	p A	sp	GTA	Val	
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	164	:					. ata	too	r act	aas	ag	c tq	c tt	t gg	c g	ag	ato	agt Ser	1588
	166	act	_ ca	g ta	t ge		, CL9	COL	, 90°	G1x	, Se	r Cv	s Ph	e Gl	y G	lu	11ϵ	e Ser	
	167	Th	c Gl	п Ту	r Ala	a Leu	ı rec	ı sei	. AIG	. 0-1		1		52	20				
	168	}		51	0				515) 	. ~~	a 22	t ca			са	act	aat	1636
	170	ate	c ct	t aa	c at	t aag	g ggc	agt	. aaa	lace	99	c aa	- A-	a A	or T	hr	Δ1ε	aat Asn	
	171	Il	e Le	u As	n Il	e Lys	s Gly	, Sei	r Lys	s Met	E GI	y AS			.9 -	111		a Asn	
	17	i at			c ct	a aa	c tac	tca	a gat	ct:	c tt	c tg	ctt	g to	cc a	ay	yaı	t gat o Asp	
	17	: u.c	0 7 r	or Se	r Le	n Gl	v Tvi	r Se	r Ası	Lei	u Ph	е Су	s Le	eu Se	er L	ys	AS	555 Asp	
		6 54				+ at			σ t.a.c	a da	t qa	t go	c aa	ag a	aa g	rtc	cta	a gaa u Glu	1732
	17	8 ct	t at	g ga	la go	- 370	g ac	~ Cl	ы ТV	r Pr	o Ās	p Āl	a Ly	ys L	ys V	al	Le	u Glu 0	ļ
	17	9 Le	u Me	et GJ	u Al	a va	T 111.	I GI	u Iy.		56	5		•			57	0	
	18	0				56	0				~ ~=	a ac	ta ci	ta c	ta c	rat	qa	g aac	1780
	18	2 ga	gag	ıg gç	gt cg	g ga	g at	CCT	c au	y aa	9 90	. 01	157 T.	21 T.	-J 2	asp	Ğl	g aac u Asn	1
	18	3 G1	u Aı	rg GI	Ly Ar	g Gl	u Il	e Le	u Me	с пу	2 01	u G	гу по	cu 1		585		u Asn	
			a σ1	α σα	ca ac	c aq	c at	g ga	g gt	c ga	c gt	g ca	ag ga	ag a	ay (JLd	. 99	g cag y Glr	,
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	18					- a+	ים מא	a ac	c tt	q ta	cac	ct c	gc t	tt g	gc (cgc	: ct	g cto u Lei	g 1876
	19	U Ct	.g g	ay d	ان مان استا	40 UL	.y yu	11 mh	r TA	u Tv	r T	nr A	rg P	he G	ly a	Arg	, Le	u Lei	1
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DATE: 05/16/2002 RAW SEQUENCE LISTING TIME: 13:22:07 PATENT APPLICATION: US/10/029,677

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05162002\J029677.raw

Output Sec. N. (one of the	
615	
192 605 GIV and one of any cag cag cag atc aca gtt	1924
194 gct gag tac acg ggg gcc cag cay aug ceu aly sign arg ile Thr Val	
195 Ala Glu Tyr Thr Gly Ala Gli Gli Lys Box - 635	
196 620 625	1972
196 620 625 198 ctg gaa acc aag atg aaa cag aac aat gaa gat gac tac ctg tct gat 198 ctg gaa acc aag atg aaa cag aac aat gaa gat gac tac ctg tct gat	
100 ton Glu Thr Lvs Met Lys Glu Ash Ash Old 101 1 2 650	
200 640 645 650 to a second se	2021
200 640 202 ggg atg aac agc cet gag etg get get gac gag eea taagacetgg 202 ggg atg aac agc cet gag etg get get gac gag eea taagacetgg	
203 Gly Met Asn Ser Pro Glu Leu Ala Ala III 1911	
204 655 660	2081
204 655 600 206 ggcccaactg cetetecage attggcettg geettgatee cagaagetag aggagetatt	2141
	2186
W> 210 tgaccetgng tttttggcct aaacatccaa gattccgcct cggat	2100
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213 <210 SEQ 15 NO. 2 214 <211> LENGTH: 664	
214 <211> DENGIN. 004	
215 <212> TYPE: PRT	
216 <213> ORGANISM: Homo sapiens	
219 <400> SEQUENCE: 2 221 Met Thr Glu Lys Thr Asn Gly Val Lys Ser Ser Pro Ala Asn Asn His	
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222 1 5 5 10 Asp His 225 Asn His His Ala Pro Pro Ala Ile Lys Ala Asn Gly Lys Asp Asp His 25 30	
225 Asn His His Ala Pro Plo Ala He Ele 25	
226 20 27 229 Arg Thr Ser Ser Arg Pro His Ser Ala Ala Asp Asp Asp Thr Ser Ser	
229 Arg Thr Ser Ser Arg Pro HIS Sel Ald Ald Alg 45	
230 35 40 230 Republic Pro Glad Glad Ser	
230 35 40 233 Glu Leu Gln Arg Leu Ala Asp Val Asp Ala Pro Gln Gln Gly Arg Ser	
234 50 55 The Arg Glu Trp Ala	
234 50 55 237 Gly Phe Arg Arg Ile Val Arg Leu Val Gly Ile Ile Arg Glu Trp Ala 75 80	
237 GIY FIRE 1129 1129 75 75 75 238 65 70 75 Pro Agn Sar Phe Leu Glu	
238 65 70 70 Asp Ser Phe Leu Glu 241 Asn Lys Asn Phe Arg Glu Glu Glu Pro Arg Pro Asp Ser Phe Leu Glu 90 95	
241 ASI 275 455 90 90 242 ASD	
242 85 245 Arg Phe Arg Gly Pro Glu Leu Gln Thr Val Thr Thr Gln Glu Gly Asp	
245 Arg the 125 100 105	
240 Gly Asp Lys Asp Gly Glu Asp Lys Gly Thr Lys Lys File	
249 GIY LYS GIY RSP LIS 120 125	
250 115 120 253 Glu Leu Phe Val Leu Asp Pro Ala Gly Asp Leu Tyr Tyr Cys Trp Leu	
253 GIU Leu Phe Vai Heu III- 140	
254 130 135 257 Phe Val Ile Ala Met Pro Val Leu Tyr Asn Trp Cys Leu Leu Val Ala	
257 Phe Val 11e Ala Met 115 Val 155	
258 145 150 258 145 261 Arg Ala Cys Phe Ser Asp Leu Gln Lys Gly Tyr Tyr Leu Val Trp Leu 170 175	
261 Arg Ala Cys Phe Sel Asp Leu 311 21 17 175 176 176 176 176 176 176 176 176 176 176	
262 165 170 Ile Ala Asp Leu Phe Ile 265 Val Leu Asp Tyr Val Ser Asp Val Val Tyr Ile Ala Asp Leu Phe Ile	
265 Val Leu Asp Tyr Val Ser Asp Val Val 191 190	
266 180 185 Leu Clu Clu Clu Clu Leu Val Lys Asp Thr	
266 180 163 269 Arg Leu Arg Thr Gly Phe Leu Glu Gln Gly Leu Leu Val Lys Asp Thr	
200 270 195 200 201 Phe Lys Leu Asp	
270 195 200 270 270 Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys Leu Asp 273 Lys Lys Leu Arg Asp Asn Tyr Ile His Thr Leu Gln Phe Lys Leu Asp 215 220	
274 210 215 The Mar Phe Ala Val Asp Ile	
274 210 215 277 Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Asp Ile 277 Val Ala Ser Ile Ile Pro Thr Asp Leu Ile Tyr Phe Ala Val Asp Ile	
277 Val Ald Sel 225 230 235 235 240	
278 225 230 278 279 279 279 279 279 279 279 279 279 279	
201 115 502	

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282 245 250 250 285 Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Asn Ty: 265		
202 Phe Glu Phe Phe Asp Arg Thr Glu Thr Arg Thr Ash Ty	r Dro	255 Asn Ile
	270	
285 PHE GIA THE 265	270 a Tla	His Tro
286 260 265 289 Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Il 289 Phe Arg Ile Ser Asn Leu Val Leu Tyr Ile Leu Val Ile	5 116	HIS ILP
289 Prie Arg 116 561 155	D =1:-	cl. Val
290 275 280 293 Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gl 293 Asn Ala Cys Ile Tyr Tyr Ala Ile Ser Lys Ser Ile Gl	y Phe	GIY VAI
293 Asn Ala Cys 11e 191 192 295		
295 294 290 295 297 Asp Thr Trp Val Tyr Pro Asn Ile Thr Asp Pro Glu Ty 310 315	r Gly	Tyr Leu
297 Asp Thr Trp Val Tyr Pro Ash Tre The 315		320
298 305 310 313 301 Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr Trp Ser Thr Le	u Thr	Leu Thr
301 Ala Arg Glu Tyr Ile Tyr Cys Leu Tyr IIp Ser 330		335
302 325 330 305 Thr Ile Gly Glu Thr Pro Pro Pro Val Lys Asp Glu Gl	n TVT	Leu Phe
205 Thr Tle Gly Glu Thr Pro Pro Pro Val Lys ASP Glu Gl	.u -1- 350)
305 111 116 617 524 345	JJO Thr	Tle Val
306 340 345 309 Val Ile Phe Asp Phe Leu Ile Gly Val Leu Ile Phe Al	rg inr	. IIC var
309 Val 11e File his 111 360	55	11- Clu
310 333 Well Cly Sor Met Ile Ser Asn Met Asn Ala Ti	ar Arg	J Ala Giu
310 355 360 313 Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Tl 313 Gly Asn Val Gly Ser Met Ile Ser Asn Met Asn Ala Tl		
375 314 370 375 317 Phe Gln Ala Lys Ile Asp Ala Val Lys His Tyr Met G. 395	ln Phe	e Arg Lys
317 Phe Gln Ala Lys Ile Asp Ala val Lys 395		400
318 385 321 Val Ser Lys Gly Met Glu Ala Lys Val Ile Arg Trp P	he Ası	p Tyr Leu
321 Val Ser Lys Gly Met Glu Ala Lys Val 116 Arg 127		415
322 Val Sel 115 327 410	AII T.V	s Asn Leu
322 405 410 325 Trp Thr Asn Lys Lys Thr Val Asp Glu Arg Glu Ile L	43	0
325 11p 111 1151 21 425	4.5	υ υ cor Thr
326 420 425 329 Pro Ala Lys Leu Arg Ala Glu Ile Ala Thr Asn Val H	is Le	u ser ini
329 Pro Ala Lys Led My 440	45	- 17-1
330 435 440 333 Leu Lys Lys Val Arg Ile Phe His Asp Cys Glu Ala G	ly Le	u Leu var
333 Leu Lys Lys Val Arg Tie The Albert 460		
334 450 455 337 Glu Leu Val Leu Lys Leu Arg Pro Gln Val Phe Ser F	ro Gl	y Asp Tyr
337 Glu Leu Val Leu Lys Leu Arg Plo Gin Val		480
338 465 470 473 341 Ile Cys Arg Lys Gly Asp Ile Gly Lys Glu Met Tyr 1	rle Il	le Lys Glu
341 The Cys Arg Lys Gly Asp The Gly Lys Glu Met 172		495
341 THE CYS MIS 212 490	າ1ກ Trt	r Ala Lei
342 485 345 Gly Lys Leu Ala Val Val Ala Asp Asp Gly Val Thr (בי די יודנ	10
345 GIY HYS HOU 500		LU Tlo Tay
346 500 505 349 Leu Ser Ala Gly Ser Cys Phe Gly Glu Ile Ser Ile :	Leu As	su tre ny.
349 Leu Ser Ald Gly Ser of 520	525	
350 515 520 353 Gly Ser Lys Met Gly Asn Arg Arg Thr Ala Asn Ile 535 540	Arg S	er Leu GI
353 Gly Ser Lys Met Gly Ash Alg My 540		
354 530 535 357 Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp Asp Leu	Met G	lu Ala Va
357 Tyr Ser Asp Leu Phe Cys Leu Ser Lys Asp 155		56
358 545 550 550 353 361 Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu 570	Ara G	lv Arg Gl
361 Thr Glu Tyr Pro Asp Ala Lys Lys Val Leu Glu Glu	Ary 0	575
361 THE GIU 191 110 111 570	17-1 7	la Thr Se
362 565 570 362 Ile Leu Met Lys Glu Gly Leu Leu Asp Glu Asn Glu 585	val A	De
365 Ile Leu Met Lys Glu GI 585	5	190
366 580 585 369 Met Glu Val Asp Val Gln Glu Lys Leu Gly Gln Leu	Glu T	hr Asn Me
oco wat clu Val Asp val Gill Giu Dio 1001	605	
369 Mer Gin var 835 var 500	Glu I	fyr Thr Gl
369 Met Giu vai ASP vai 511 600 600 370 595 600 Arg Leu Ala		_
370 595 373 Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala		
370 595 373 Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala	Glu ⁿ	thr Lvs Me
370 595 373 Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala	Glu 1	Thr Lys Me
370 595 373 Glu Thr Leu Tyr Thr Arg Phe Gly Arg Leu Leu Ala	Glu T	Thr Lys Me 64

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Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 2150

VERIFICATION SUMMARY

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L:12 M:283 W: Missing Blank Line separator, <140> field identifier L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:2141